



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 146887**

**TO: Emily M Le**  
**Location: 3c35/3c18**  
**Art Unit: 1648**  
**Thursday, March 10, 2005**

**Case Serial Number: 09/939537**

**From: Noble Jarrell**  
**Location: Biotech-Chem Library**  
**Rem 1B71**  
**Phone: 272-2556**

**Noble.jarrell@uspto.gov**

### **Search Notes**

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2005, 06:29:55 ; Search time 3106 Seconds  
(without alignments)  
9411.899 Million cell updates/sec

Title: US-09-939-537-32

Perfect score: 768  
Sequence: 1 GGTAGCAGAGCCCAATCTT.....GGCTCTGACGACGATCC 768

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gss1:\*

9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736.6	95.9	881	5 BQ711291	BQ711291 AGENCOURT
2	691.2	90.0	871	4 BG753979	BG753979 602709506
3	691.2	90.0	983	5 BQ708975	BQ708975 AGENCOURT
4	690.2	89.9	897	5 BQ709144	BQ709144 AGENCOURT
5	690.2	89.9	941	5 BQ712021	BQ712021 AGENCOURT
6	689.6	89.8	843	4 BM007897	BM007897 603617582
7	689.6	89.8	925	5 BQ709152	BQ709152 AGENCOURT
8	689.6	89.8	1022	3 CR611254	CR611254 full-leng
9	689.6	89.8	1048	3 CR595172	CR595172 full-leng
10	689.6	89.8	1090	3 CR612308	CR612308 full-leng
11	689.6	89.8	1093	3 CR604961	CR604961 full-leng
12	689.6	89.8	1093	3 CR616804	CR616804 full-leng
13	689.6	89.8	1098	3 CR626477	CR626477 full-leng
14	689.6	89.8	1100	3 CR612813	CR612813 full-leng
15	689.6	89.8	1102	3 CR601777	CR601777 full-leng
16	689.6	89.8	1102	3 CR625051	CR625051 full-leng
17	689.6	89.8	1103	3 CR595194	CR595194 full-leng
18	689.6	89.8	1104	3 CR591904	CR591904 full-leng
19	689.6	89.8	1106	3 CR613460	CR613460 full-leng
20	689.6	89.8	1106	3 CR620071	CR620071 full-leng
21	689.6	89.8	1107	3 CR598548	CR598548 full-leng
22	689.6	89.8	1109	3 CR614200	CR614200 full-leng
23	689.6	89.8	1109	3 CR619687	CR619687 full-leng
24	689.6	89.8	1111	3 CR606782	CR606782 full-leng

25	689.6	89.8	1114	3 CR593349	CR593349 full-leng
26	689.6	89.8	1114	3 CR618075	CR618075 full-leng
27	689.6	89.8	1118	3 CR613511	CR613511 full-leng
28	689.6	89.8	1120	3 CR619868	CR619868 full-leng
29	689.6	89.8	1124	3 CR611468	CR611468 full-leng
30	689.6	89.8	1126	3 CR598462	CR598462 full-leng
31	689.6	89.8	1142	3 CR598316	CR598316 full-leng
32	689.6	89.8	1179	3 CR607277	CR607277 full-leng
33	689.6	89.8	1287	3 CR611016	CR611016 full-leng
34	689.6	89.8	1289	3 CR594000	CR594000 full-leng
35	688.6	89.7	851	5 BX346946	BX346946 BX346946
36	688.6	89.7	973	5 BQ706204	BQ706204 AGENCOURT
37	688.6	89.6	919	5 BQ709339	BQ709339 AGENCOURT
38	686.4	89.4	947	5 BQ709771	BQ709771 AGENCOURT
39	685.8	89.3	856	5 BQ709859	BQ709859 AGENCOURT
40	685.4	89.2	914	5 BQ712363	BQ712363 AGENCOURT
41	684.2	89.1	1013	5 BX360518	BX360518 BX360518
42	683.8	89.0	757	4 BG674795	BG674795 602620925
43	683.2	89.0	902	5 BUI46962	BUI46962 AGENCOURT
44	679.2	88.4	892	4 BG397723	BG397723 603438784
45	679.2	88.4	897	4 BM008412	BM008412 603617406

#### ALIGNMENTS

RESULT 1  
BQ711291  
LOCUS BQ711291 881 bp mRNA linear EST 16-JUL-2002  
DEFINITION AGENCOURT\_8347186 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6279096  
5', mRNA sequence.  
ACCESSION BQ711291  
VERSION BQ711291  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 881)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLCM2468 row: c column: 01  
High quality sequence stop: 721.  
Location/Qualifiers  
source 1. .881  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6279096"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 113"  
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACAGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

#### ORIGIN

Query Match 95.9%; Score 736.6; DB 5; Length 881;  
Best Local Similarity 98.2%; Pred. No. 8.4e-169;

	Matches	745;	Conservative	0;	Mismatches	14;	Indels	0;	Gaps	0;
QY	4	AGCAGAGCCCAAAATCTTTGTGCACAAAAC	TCA	CATGCCCCACCGTGC	CCAGCACTGAACT	63				
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QY	64	CTTGGGGGACCGTCAAGTCTTCTTCTTCCCCCAAAA	CCC	AAGGACACCCCTCATGATCTC	123					
Db	178	CTTGGGGGACCGTCAAGTCTTCTTCTTCCCCCAAAA	CCC	AAGGACACCCCTCATGATCTC	237					
QY	124	CCGAGCCCTGAGGTCACATGCGTGTGTGTGTGAC	CTG	TGACCAAGAACCCCTGAGGTCAA	183					
Db	238	CCGAGCCCTGAGGTCACATGCGTGTGTGTGTGAC	CTG	TGACCAAGAACCCCTGAGGTCAA	297					
QY	184	GTTCAA	CTGT	TACGTGGACGGCGTGGAGGTGCATTAATGCC	AAGCAAGCCGCGGGAGGA	243				
Db	298	GTTCAA	CTGT	TACGTGGACGGCGTGGAGGTGCATTAATGCC	AAGCAAGCCGCGGGAGGA	357				
QY	244	GCAGTACACAGCAGTAC	CGGGTGGT	CAGCGTCTCTACCGTCTCTG	CACCAAGGACTTGGCT	303				
Db	358	GCAGTACACAGCAGTAC	CGGGTGGT	CAGCGTCTCTACCGTCTCTG	CACCAAGGACTTGGCT	417				
QY	304	GAATGCGAAGGAGTACAAAGTGC	AAGTCTCCAA	CAAAAGCCCTCCGACGCCCAATGAGAA	363					
Db	418	GAATGCGAAGGAGTACAAAGTGC	AAGTCTCCAA	CAAAAGCCCTCCGACGCCCAATGAGAA	477					
QY	364	AACCATCTCCAAAGCCAAAGGGCAG	CCCCCGAGAACCA	CAGGTGTATACCCCTGCCCCCATC	423					
Db	478	AACCATCTCCAAAGCCAAAGGGCAG	CCCCCGAGAACCA	CAGGTGTATACCCCTGCCCCCATC	537					
QY	424	CCGGATCAGCTGACCAAGAC	CAGGTACGCTTG	CTTGGTCAAGGGTCTTATCC	483					
Db	538	CCGGATCAGCTGACCAAGAC	CAGGTACGCTTG	CTTGGTCAAGGGTCTTATCC	597					
QY	484	CAGCGACATCGCCGTGGAGTGGGAGAGCAAT	GGCAGCCGAGAGAC	CACTACAGACCAAC	543					
Db	598	CAGCGACATCGCCGTGGAGTGGGAGAGCAAT	GGCAGCCGAGAGAC	CACTACAGACCAAC	657					
QY	544	GCCTCCCGTGTGACCTCGAC	CGGCTCTTCTTCTCTACACAAAGCT	CACCGGTGGACAA	603					
Db	658	GCCTCCCGTGTGACCTCGAC	CGGCTCTTCTTCTCTACACAAAGCT	CACCGGTGGACAA	717					
QY	604	GAGCAGGTGGCAGCAGGGGAACTCTTCTTCATGCT	CCGCTGATGCA	TGAGGCTCTGCAAA	663					
Db	718	GAGCAGGTGGCAGCAGGGGAACTCTTCTTCATGCT	CCGCTGATGCA	TGAGGCTCTGCAAA	777					
QY	664	CCACTACACGAGAGAGCTCTTCCGTGTCTCCGGGGCT	GCACCTGACAGACGACTGTGC	723						
Db	778	CCACTACACGAGAGAGCTCTTCCGTGTCTCCGGGGCT	GCACCTGACAGACGACTGTGC	787						
QY	724	TGAGGCCCAAGGACGGGGAGCTGGA	CGGGCTGTGACGAC	762						
Db	838	GGAGCGCAGGAAACGGGAGCTGGAC	CGGGCTGTGACGAC	876						

RESULT 2	871 bp	mRNA	linear	EST 15-MAY-2001		
LOCUS	60270950506F1	NIH_MGC_48	Homo sapiens	cDNA clone IMAGE:4846201 5',		
DEFINITION	mRNA sequence.					
ACCESSION	BG753979					
VERSION	BG753979					
KEYWORDS	EST.					
SOURCE	BG753979.1	GI:14064632				
ORGANISM	Homo sapiens (human)					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
REFERENCE	1 (bases 1 to 871)					
AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/.				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Robert Strausberg, Ph.D.					
	Email: cgaabs-r@mail.nih.gov					

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCMI686 row: k column: 02  
High quality sequence stop: 848.  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/clone="IMAGE:4846201"  
/tissue\_type="primary B-cells from tonsils (cell line)"  
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/clone\_lib="NIH\_MGC\_48"  
/note="Organ: B-cells; Vector: pOTE7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGACGAG(G). Size-selected 500bp  
for average insert size 1.8kb. Library constructed by Ling  
Hong in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: This is a NIH MGC Library."

## ORIGIN

Query Match	90.0%;	Score 691.2;	DB 4;	Length 871;
Best Local Similarity	99.6%;	Pred. No. 9.9e-158;		
Matches 693;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	4	AGCAGAGCCAAATCTTGTGACAAAACCTCACACATGCCACCGTGGCCAGCAGCACTGAACT	63	
Db	18	AGTTGAGCCCAAACTTGTGACAAAACCTCACACATGCCACCGTGGCCAGCAGCACTGAACT	77	
QY	64	CTGTGGGGGACCGTCAGTCTTCTTCCGCCCAAAACCCCAAGGACACCCCTCATGATCTC	123	
Db	78	CTTGGGGGACCGTCAGTCTTCTTCCGCCCAAAACCCCAAGGACACCCCTCATGATCTC	137	
QY	124	CCGGACCCCTGAGGTCAATGCGTGGTGGTGGACGTCGAGCCACGAAGACCCCTGAGGTCAA	183	
Db	138	CCGGACCCCTGAGGTCAATGCGTGGTGGTGGACGTCGAGCCACGAAGACCCCTGAGGTCAA	183	
QY	184	GTTCAACTGGTACGTGTGACCGCGTGGAGGTGCATATGCGACAAAGCCGCGGAGGA	243	
Db	198	GTTCAACTGGTACGTGTGACCGCGTGGAGGTGCATATGCGACAAAGCCGCGGAGGA	257	
QY	244	GCAGTCAACAGCACAGTACCGGGTGTGACGGTCTCTCAACGAGCCCTCTGACACGAGCTGGCT	303	
Db	258	GCAGTCAACAGCACAGTACCGGGTGTGACGGTCTCTCAACGAGCCCTCTGACACGAGCTGGCT	317	
QY	304	GAATGGCAAGGATCAAGGTGCAAGGTCTTCAACAAAGCCCTCCACAGCCCGCATCGAGAA	363	
Db	318	GAATGGCAAGGATCAAGGTGCAAGGTCTTCAACAAAGCCCTCCACAGCCCGCATCGAGAA	377	
QY	364	AACCAATCTCAAAGCCAAAGGCGACCCCGAGAAACACAGGTGTATCACCTGCCCCCATC	423	
Db	378	AACCAATCTCAAAGCCAAAGGCGACCCCGAGAAACACAGGTGTATCACCTGCCCCCATC	437	
QY	424	CCGGATGAGCTGACGACGAACCAAGTCAGCTGACCTGCTGGTTCAAAGGCTTCTATCC	483	
Db	438	CCGGATGAGCTGACGACGAACCAAGTCAGCTGACCTGCTGGTTCAAAGGCTTCTATCC	497	
QY	484	CAGCGACATCGCTGGAGTGGGAGAGCAATGGGCGAGCCGAGAACACACTACAGACCA	543	
Db	498	CAGCGACATCGCTGGAGTGGGAGAGCAATGGGCGAGAACACACTACAGACCA	557	
QY	544	GCCTCCCGTGTGGACTCCGAGGCTCTTCTTCTTCTATCAGGAGCTCACCGTGGACAA	603	
Db	558	GCCTCCCGTGTGGACTCCGAGGCTCTTCTTCTTCTTCTATCAGGAGCTCACCGTGGACAA	617	

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QY 604 GAGCAGGTGGCAGCAGGGGAAAGCTTCTCTCAGTCTCCGTGATGATGAGGCTCTGCACAA 663
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DB 618 GAGCAGGTGGCAGCAGGGGAAAGCTTCTCTCAGTCTCCGTGATGATGAGGCTCTGCACAA 677
|||
QY 664 CCACTACACGACAGAGAGCTCTCCCTGCTCCGGG 699
|||
DB 678 CCACTACACGACAGAGAGCTCTCCCTGCTCCGGG 713
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RESULT 3
BQ708975 983 bp mRNA linear EST 16-JUL-2002
LOCUS AGENCOURT_8353514 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279683
DEFINITION 5', mRNA sequence.
ACCESSION BQ708975
VERSION BQ708975.1 GI:21847874
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgs.nci.nih.gov/.
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2459 row: k column: 12
High quality sequence stop: 604.
Location/Qualifiers
1..983
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:6279683"
/lab_host="NIH MGC 113"
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCACGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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## ORIGIN

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Query Match 90.0%; Score 691.2; DB 5; Length 983;
Best Local Similarity 99.6%; Pred. No. 1e-157;
Matches 693; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTGCAAAACTCACATGCCCCCAGGACACCTCATGATCTC 123
DB 5 AGTTGAGCCCAATCTTGTGCAAAACTCACATGCCCCCAGGACACCTCATGATCTC 64
QY 64 CTGGGGGACCGTCACTCTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTC 123
DB 65 CTGGGGGACCGTCACTCTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTC 124
QY 124 CCGGACCCCTGAGGTCAATGCGTGTGTGTGAGCGTGCACGAGACCCCTGAGGTCAA 183
DB 125 CCGGACCCCTGAGGTCAATGCGTGTGTGTGAGCGTGCACGAGACCCCTGAGGTCAA 184
QY 184 GTTCACTGTGTAGTGGAGCGGTGTGAGTGCATATGTCACAGACAAACCGCGGAGGA 243
DB 185 GTTCACTGTGTAGTGGAGCGGTGTGAGTGCATATATGCCAAGACAAACCGCGGAGGA 244
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QY 304 GAATGGCAAGGAGTACAGTGCAGAGGTCTCCCAACAAAGCCCTCCCAAGCCCCCATCGAGAA 363
DB 305 GAATGGCAAGGAGTACAGTGCAGAGGTCTCCCAACAAAGCCCTCCCAAGCCCCCATCGAGAA 364
QY 364 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACACACAGGTGTACACCTTGCCCCCATC 423
DB 365 AACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACACACAGGTGTACACCTTGCCCCCATC 424
QY 424 CCGGATGAGTGCACCAAGAACAGGTGACCTGACCTGCTCGCTGGTCAAGGGCTTCTATCC 483
DB 425 CCGGATGAGTGCACCAAGAACAGGTGACCTGACCTGCTCGCTGGTCAAGGGCTTCTATCC 484
QY 484 CAGCGACATCGCGTGGAGTGGAGGAGCAATGGGAGCCGCGAGAACCACTACAAGACCAC 543
DB 485 CAGCGACATCGCGTGGAGTGGAGGAGCAATGGGAGCCGCGAGAACCACTACAAGACCAC 544
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QY 604 GAGCAGGTGGCAGCAGGGGAAAGCTTCTCATGCTCCCGTATGATGAGGCTCTGCACAA 663
DB 605 GAGCAGGTGGCAGCAGGGGAAAGCTTCTCATGCTCCGCTGATGATGAGGCTCTGCACAA 664
QY 664 CCACCTACGCGAGAGAGCCCTCTCCCTGCTCCGGG 699
DB 665 CCACCTACGCGAGAGAGCCCTCTCCCTGCTCCGGG 700
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## RESULT 4

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BQ709144 897 bp mRNA linear EST 16-JUL-2002
LOCUS AGENCOURT_8474994 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301566
DEFINITION 5', mRNA sequence.
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## ACCESSION

BQ709144

## VERSION

BQ709144.1 GI:21848043

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 897)

## AUTHORS

NIH-MGC http://mgs.nci.nih.gov/.

## TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2517 row: k column: 07

High quality sequence stop: 626.

## FEATURES

Location/Qualifiers

1..897

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6301566"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 113"

/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCAGAG(G). Library constructed by Ling Hong in the

laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 89.9%; Score 690.2; DB 5; Length 897;  
Best Local Similarity 99.6%; Pred. No. 1.7e-157;  
Matches 692; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTGTGACAAAATCTCACATGCCACCGTGCAGCAGCACTGAAT 63  
Db 31 AGTTGAGCCCAATCTGTGACAAAATCTCACATGCCACCGTGCAGCAGCACTGAAT 90

QY 64 CTTGGGGGAGCCGTGAGTCTTCTCTTCCCTCCAAACCCAGGACACCTCATGATCTC 123  
Db 91 CTTGGGGGAGCCGTGAGTCTTCTCTTCCCTCCAAACCCAGGACACCTCATGATCTC 150

QY 124 CCGGACCCCTGAGGTACATGCGTGGTGGACGTGAGCCACGAGACCCCTGAGGTCAA 183  
Db 151 CCGGACCCCTGAGGTACATGCGTGGTGGACGTGAGCCACGAGACCCCTGAGGTCAA 210

QY 184 GTTCAACTGCTGAGTGGAGCGGCTGAGGTGATATGCGCAAGACCAAGCCGCGGAGGA 243  
Db 211 GTTCAACTGCTGAGTGGAGCGGCTGAGGTGATATGCGCAAGACCAAGCCGCGGAGGA 270

QY 244 GCAGTACACAGCAGTACCGGGTGGTCAAGCTCTTCCCTGTCACACGAGCACTGGCT 303  
Db 271 GCAGTACACAGCAGTACCGGGTGGTCAAGCTCTTCCCTGTCACACGAGCACTGGCT 330

QY 304 GAATGGCAAGGAGTACAAAGTCCAAAGTCTTCCCTCCAAACCCAGGACACCTCATGATCTC 363  
Db 331 GAATGGCAAGGAGTACAAAGTCTTCCCTCCAAACCCAGGACACCTCATGATCTC 390

QY 364 AACCATCTCCAAAGCAAGGCGAGCCCGGAGAACCAAGGTGTACACCTGCCCCCATC 423  
Db 391 AACCATCTCCAAAGCAAGGCGAGCCCGGAGAACCAAGGTGTACACCTGCCCCCATC 450

QY 424 CCGGATGAGTGTGACCAAGAACCAAGTCCAGCTGAGCTGAGCTGCTGCAAGGCTTCTATCC 483  
Db 451 CCGGATGAGTGTGACCAAGAACCAAGTCCAGCTGAGCTGAGCTGCTGCAAGGCTTCTATCC 510

QY 484 CAGCGACATCCCGTGGAGTGGAGAGCAATGGGCAACCGGAGAACCACTACAGACCAAC 543  
Db 511 CAGCGACATCCCGTGGAGTGGAGAGCAATGGGCAACCGGAGAACCACTACAGACCAAC 570

QY 544 GCCTCCCGTGGTGGACTCCGAGCGCTCTTCTTCTTCTACGCAAGCTCCCGTGGACAA 603

RESULT 5

BQ712021  
LOCUS BQ712021 941 bp mRNA linear EST 16-JUL-2002  
DEFINITION AGENCOURT\_8418162 NIH\_MGC\_113 Homo sapiens cDNA clone IMAGE:6281403  
5', mRNA sequence.  
ACCESSION BQ712021  
VERSION BQ712021.1 GI:21850920  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 941)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE  
JOURNAL  
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
clone distribution: Agencourt Bioscience Corporation  
found through the I.M.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM2474 row: c column: 04  
High quality sequence stop: 638.

FEATURES  
source

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/clone="IMAGE:6281403"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_113"  
/note="organ: spleen; Vector: pOTB7; Site:1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GcCAGAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

ORIGIN

Query Match 89.9%; Score 690.2; DB 5; Length 941;  
Best Local Similarity 99.4%; Pred. No. 1.8e-157;  
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTGACAAAATCTCACATGCCACCGTGCAGCAGCACTGAAT 63  
Db 31 AGTTGAGCCCAATCTTGTGACAAAATCTCACATGCCACCGTGCAGCAGCACTGAAT 90

QY 64 CTTGGGGGAGCCGTGAGTCTTCTTCCCTCCAAACCCAGGACACCTCATGATCTC 123  
Db 91 CTTGGGGGAGCCGTGAGTCTTCTTCCCTCCAAACCCAGGACACCTCATGATCTC 150

QY 124 CCGGACCCCTGAGTGCATGCGTGGTGGAGCTGAGCCAGAGACCTGAGGTCAA 183  
Db 151 CCGGACCCCTGAGTGCATGCGTGGTGGAGCTGAGCCAGAGACCTGAGGTCAA 210

QY 184 GTTCAACTGCTGAGTGGAGCGGCTGAGGTGATATGCGCAAGACCAAGCCGCGGAGGA 243  
Db 211 GTTCAACTGCTGAGTGGAGCGGCTGAGGTGATATGCGCAAGACCAAGCCGCGGAGGA 270

QY 244 GCAGTACACAGCAGTACCGGGTGGTCAAGCTCTTCCCTGTCACACGAGCTGGCT 303  
Db 271 GCAGTACACAGCAGTACCGGGTGGTCAAGCTCTTCCCTGTCACACGAGCTGGCT 330

QY 304 GAATGGCAAGGAGTACAAAGTCCAAAGTCTTCCCTCCAAACCCAGGACACCTCATGATCTC 363  
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QY 364 AACCATCTCCAAAGCAAGGCGAGCCCGGAGAACCAAGGTGTACACCTGCCCCCATC 423  
Db 391 AACCATCTCCAAAGCAAGGCGAGCCCGGAGAACCAAGGTGTACACCTGCCCCCATC 450

QY 424 CCGGATGAGTGTGACCAAGAACCAAGTCCAGCTGAGCTGAGCTGCTGCAAGGCTTCTATCC 483  
Db 451 CCGGATGAGTGTGACCAAGAACCAAGTCCAGCTGAGCTGAGCTGCTGCAAGGCTTCTATCC 510

QY 484 CAGCGACATCCCGTGGAGTGGAGAGCAATGGGCAACCGGAGAACCACTACAGACCAAC 543  
Db 511 CAGCGACATCCCGTGGAGTGGAGAGCAATGGGCAACCGGAGAACCACTACAGACCAAC 570

QY 544 GCCTCCCGTGGTGGACTCCGAGCGCTCTTCTTCTTCTACGCAAGCTCCCGTGGACAA 603







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Db      904 GAGCAGGTGGCAGCGGGAACGCTTCTCATGCTCCGTCATGTCATGAGGCTCTGCACAA 963
QY      664 CCCTACACGACGAGAGAGCTCTCCCTGCTCTCGGG 699
Db      964 CCCTACACACAGAGAGGCTCTCCCTGCTCTCGGG 999

RESULT 9
LOCUS   CR595172 1048 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0D1040YA16 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR595172
VERSION 1
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1048)
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1048)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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Query Match 89.8%; Score 689.6; DB 3; Length 1048;
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Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4 AGCAGGCCCAATCTTGACAAACTCACATATGCCACCGTCCCGACCTGAACT 63
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QY      64 CTGCGGGGACCGTCAGTCTTCTTCCGCCCAAAACCCAAAGCACACCTCATGATCTC 123
Db      377 CTGCGGGGACCGTCAGTCTTCTTCCGCCCAAAACCCAAAGCACACCTCATGATCTC 436
QY      124 CCGGACCCCTGAGGTCACATGCGTGGTGTGACCGTACGACCGACGAGACCTTGAGGTCAA 183
Db      437 CCGGACCCCTGAGGTCACATGCGTGGTGTGACCGTACGACCGACGAGACCTTGAGGTCAA 496
QY      184 GTTCAACTGGTACGTGGACGGCTGGAGTGATATGTCACAGCAAAAGCCCGGGAGGA 243
Db      497 GTTCAACTGGTACGTGGACGGCTGGAGTGATATGTCACAGCAAAAGCCCGGGAGGA 556
QY      244 GCAGTACAAACAGACGCTACCGGGTGGTCAAGCGTCTCACCCTGCTGACACGAGCTGGCT 303
Db      557 GCAGTACAAACAGACGCTACCGGGTGGTCAAGCGTCTCACCCTGCTGACACGAGCTGGCT 616
QY      304 GAATGGCAAGGAGTACAAGTGCAGAGTCTTCCAAAGCCCTCCAGCCCCCATCGAGAA 363

Db      617 GAATGGCAAGGAGTACAAGTGCAGAGTCTCCAAAGCCCTCCAGCCCCCATCGAGAA 676
QY      364 AACCATCTCCAAAGCAAAAGGCGAGCCCGGAGAACACAGAGGTGTACACCTGCCCCATC 423
Db      677 AACCATCTCCAAAGCAAAAGGCGAGCCCGGAGAACACAGAGGTGTACACCTGCCCCATC 736
QY      424 CCGGATGAGCTGACCAAGAACAGGTGAGCTGACCTGCTGCTGCTCAAGGGCTTCTATCC 483
Db      737 CCGGATGAGCTGACCAAGAACAGGTGAGCTGAGCTGACCTGCTGCTCAAGGGCTTCTATCC 796
QY      484 CAGCCACATCCCGTGGAGTGGAGAGCAATGGGCGAGCCGGAGAACACTACAAGACCAAC 543
Db      797 CAGCCACATCCCGTGGAGTGGAGAGCAATGGGCGAGCCGGAGAACACTACAAGACCAAC 856
QY      544 GCCTCCCGTGTGGAGTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAA 603
Db      857 GCCTCCCGTGTGGAGTCCGACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAA 916
QY      604 GAGCAGGTGGCAGCAGGGAAGCTTCTTCTATGCTCCGTCGTCATGAGGCTCTGCACAA 663
Db      917 GAGCAGGTGGCAGCAGGGAAGCTTCTTCTATGCTCCGTCGTCATGAGGCTCTGCACAA 976
QY      664 CCACTACACGACAGAGCGCTCTCCCTGCTCTCCGG 699
Db      977 CCACTACACACAGAGCGCTCTCCCTGCTCTCCGG 1012

RESULT 10
LOCUS   CR612308 1090 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0D1071YG21 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR612308
VERSION 1
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1090)
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1090)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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1..1090
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/mol_type="mRNA"
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/clone="CS0D1071YG21"
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ORIGIN
Query Match 89.8%; Score 689.6; DB 3; Length 1090;
Best Local Similarity 99.4%; Pred. No. 2.5e-157;
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4 AGCAGGCCCAATCTTGTCGACAAACTCTTGTGTGACAAACTCACATATGCCACCGTCCCGACCTGAACT 63
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Db	304	AGTTGAGCCCAAACTTTGTGCAAAACTCACATATGCCACCGTGCCAGCACCTGAAC	363
Qy	64	CCTGGGGGACCGTCAGTCTTCTCTTCCCGCCAAACCCAAAGACACCCCTCATGATCTC	123
Db	364	CCTGGGGGACCGTCAGTCTTCTCTTCCCGCCAAACCCAAAGACACCCCTCATGATCTC	423
Qy	124	CCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTGAGCCACGAAGACCCCTGAGGTCAA	183
Db	424	CCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTGAGCCACGAAGACCCCTGAGGTCAA	483
Qy	184	GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAGCGCGGGAGGA	243
Db	484	GTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAGCGCGGGAGGA	543
Qy	244	GCAGTACAAACAGCACGTACCGGGTGGTCAAGGTCTCACCGTCTCTGCACCAAGACTTGGCT	303
Db	544	GCAGTACAAACAGCACGTACCGGTGGTCAAGGTCTCACCGTCTCTGCACCAAGACTTGGCT	603
Qy	304	GAATGGCAAGGAGTCAAGTGCAGAGTCTTCAACAAGAGCCCTCCAGCCCCCATCGAGAA	363
Db	604	GAATGGCAAGGAGTCAAGTGCAGAGTCTTCAACAAGAGCCCTCCAGCCCCCATCGAGAA	663
Qy	364	AACCATCTCCAAAGCCAAAGGCGACCCCGGAGAACCAAGGTGTACACCTTGCSCCCATC	423
Db	664	AACCATCTCCAAAGCCAAAGGCGACCCCGGAGAACCAAGGTGTACACCTTGCSCCCATC	723
Qy	424	CCGGATGAGCTGACCAAGAACCAAGTCAAGTCTGACCTGCTTGTCAAAGGCTTCTATCC	483
Db	724	CCGGATGAGCTGACCAAGAACCAAGTCAAGTCTGACCTGCTTGTCAAAGGCTTCTATCC	783
Qy	484	CAGCGACATCGCGTGGAGTGGGAGACAAATGGGCGCCGAGAACAACTACAAGACCA	543
Db	784	CAGCGACATCGCGTGGAGTGGGAGACAAATGGGCGCCGAGAACAACTACAAGACCA	843
Qy	544	GCCTCCGGTCTTGAACTCCGACGGCTCTTCTTCTTCTTACAGCAAGCTCACCGTGAACAA	603
Db	844	GCCTCCGGTCTTGAACTCCGACGGCTCTTCTTCTTCTTACAGCAAGCTCACCGTGAACAA	903
Qy	604	GAGCAGGTGGCAGCAGGGGAAAGTCTTCTCATGTCCGTGATGATGAGGCTCTGCACAA	663
Db	904	GAGCAGGTGGCAGCAGGGGAAAGTCTTCTCATGTCCGTGATGATGAGGCTCTGCACAA	963
Qy	664	CCAATAACGCGAAGAGAGCTCTCCCTGTCTCCGGG	699
Db	964	CCAATAACGCGAAGAGAGCTCTCCCTGTCTCCGGG	999

RESULT 11	
CR604961	1091 bp mRNA linear HTC 21-JUL-2004
LOCUS	
DEFINITION	full-length cDNA clone CSODI009Y710 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION	CR604961
VERSION	CR604961.1 GI:50485768
KEYWORDS	HTC; CNSLT CDNA.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1091)
TITLE	Li, W.B., Gruber, C., Jesses, J. and Polayes, D.
JOURNAL	Full-length cDNA libraries and normalization
REMARK	Unpublished
	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue
REFERENCE	2 (bases 1 to 1091)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.									
FEATURES	Location/Qualifiers									
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Best Local Similarity	99.4%;	Pred. No.	2.5e-157;							
Matches	692;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;	

RESULT 12	LOCUS	DEFINITION
CR616804		

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ACCESSION CR616804
VERSION CR616804.1 GI:50497611
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1093)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1093)
REFERENCE 2 (bases 1 to 1093)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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Best Local Similarity 99.4%; Pred. No. 2.5e-157;
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 AGCAGAGCCCAATCTTGTGACAAAACCTCACACATGCGCCACGTCGCCAGACCTGGAACCT 63
DB 304 AGTTGAGCCCAATCTTGTGACAAAACCTCACACATGCGCCACGTCGCCAGACCTGGAACCT 363
QY 64 CTGGGGGACCGTCAGTCTTCTCTTCCCTCCCAAAACCCAAAGGACACCTCATGATCTC 123
DB 364 CTGGGGGACCGTCAGTCTTCTCTTCCCTCCCAAAACCCAAAGGACACCTCATGATCTC 423
QY 124 CCGGACCCCTGAGGTACATGCGTGGTGGAGCGGACCGTGGAGGACACCTCATGATCTC 183
DB 424 CCGGACCCCTGAGGTACATGCGTGGTGGAGCGGACCGTGGAGGACACCTCATGATCTC 483
QY 184 GTTCAACTGGTACGTGGAGGACCAATGGGACCGCGGAGAACCACTACAAGCCGCGGAGGA 243
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Best Local Similarity 99.4%; Pred. No. 2.5e-157;
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 64 CTGGGGGACCGTCAGTCTTCTCTTCCCTCCCAAAACCCAAAGGACACCTCATGATCTC 123
DB 364 CTGGGGGACCGTCAGTCTTCTCTTCCCTCCCAAAACCCAAAGGACACCTCATGATCTC 423
QY 124 CCGGACCCCTGAGGTACATGCGTGGTGGAGCGGACCGTGGAGGACACCTCATGATCTC 183
DB 424 CCGGACCCCTGAGGTACATGCGTGGTGGAGCGGACCGTGGAGGACACCTCATGATCTC 483
QY 184 GTTCAACTGGTACGTGGAGGACCAATGGGACCGCGGAGAACCACTACAAGCCGCGGAGGA 243
ACCESSION CR616804
VERSION CR616804.1 GI:50497611
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1093)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1093)
REFERENCE 2 (bases 1 to 1093)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
Location/Qualifiers
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/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Query Match 89.8%; Score 689.6; DB 3; Length 1093;
Best Local Similarity 99.4%; Pred. No. 2.5e-157;
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 4 AGCAGAGCCCAATCTTGTGACAAAACCTCACACATGCGCCACGTCGCCAGACCTGGAACCT 63
DB 304 AGTTGAGCCCAATCTTGTGACAAAACCTCACACATGCGCCACGTCGCCAGACCTGGAACCT 363
QY 64 CTGGGGGACCGTCAGTCTTCTCTTCCCTCCCAAAACCCAAAGGACACCTCATGATCTC 123
DB 364 CTGGGGGACCGTCAGTCTTCTCTTCCCTCCCAAAACCCAAAGGACACCTCATGATCTC 423
QY 124 CCGGACCCCTGAGGTACATGCGTGGTGGAGCGGACCGTGGAGGACACCTCATGATCTC 183
DB 424 CCGGACCCCTGAGGTACATGCGTGGTGGAGCGGACCGTGGAGGACACCTCATGATCTC 483
QY 184 GTTCAACTGGTACGTGGAGGACCAATGGGACCGCGGAGAACCACTACAAGCCGCGGAGGA 243
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Db 484 GTTCACTGGTACGTGACGGCTGGAGGTGCATATGCCAAGACAAAGCCGCGGAGGA 543
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Qy 304 GAATGGCAAGGAGTACAAAGTGCAGAGTCTCCAAACAAAGCCCTCCAGCCGCCATCGAGAA 363
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Db 664 AACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGTGTACACCCCTGCCCCCATC 723
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Db 724 CCGGATGAGTGCACCAAGAACCAAGGTCAGCTGACCTGCTGGTCAAAAGGCTTCTATCC 783
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Db 784 CAGCAGATCCCGTGGAGTGGGAGAGCAATGGGCGAGCCGAGAAACAATCAAGACCCAC 843
Qy 544 GCCTCCCGTGGTGAATCCGACCGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAA 603
Db 844 GCCTCCCGTGGTGAATCCGACCGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAA 903
Qy 604 GAGCAGTGGCAGCAGGCGGAACGTCTCTCATGCTCCGATGATGAGGCTCTGCACAA 663
Db 904 GAGCAGTGGCAGCAGGCGGAACGTCTCTCATGCTCCGATGATGAGGCTCTGCACAA 963
Qy 664 CCACCTACACAGAGAGAGCTCTCCCTGTCTCCGGG 699
Db 964 CCACCTACACAGAGAGAGCTCTCCCTGTCTCCGGG 999

RESULT 14
CR612813
LOCUS full-length cDNA clone CSOD1081F02 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR612813
VERSION 1 GI:50493620
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Li W.B., Gruber,C., Jessee,J. and Polayes,D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1100)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source
1..1100
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## ORIGIN

Query Match 89.8%; Score 689.6; DB 3; Length 1100;  
Best Local Similarity 99.4%; Pred. No. 2.5e-157;  
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 300 AGTTGAGCCCAATCTTTGTGACAAAATCACAATGCCCCACCGTCCCGACGACCTGAACT 359
Qy 64 CTTGGGGGGACCGTCAAGTCTTCTTCCCCCAAAACCCCAAGGACACCTCATGATCTC 123
Db 360 CTTGGGGGGACCGTCAAGTCTTCTTCCCCCAAAACCCCAAGGACACCTCATGATCTC 419
Qy 124 CCGGACCCCTGAGGTGCATGCTGCTGGTGGACGTGAGCCAGCAAGACCTTGAAGTCAA 183
Db 420 CCGGACCCCTGAGGTGCATGCTGCTGGTGGACGTGAGCCAGCAAGACCTTGAAGTCAA 479
Qy 184 GTTCAACTCTGACGTGGACGGGTGGAGTGCATAATGCCAAGACAAAGCCGCGGAGGA 243
Db 480 GTTCAACTCTGACGTGGACGGGTGGAGTGCATAATGCCAAGACAAAGCCGCGGAGGA 539
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Db 540 GCAGTACAAACAGACAGTACCGGGTGGTCAAGTCTCTCAACCGTCTGACACGAGACTGGCT 599
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Db 600 GAATGGCAAGGAGTACAAAGTGCAGAGTCTCCAAACAAAGCCCTCCAGCCGCCATCGAGAA 659
Qy 364 AACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGTGTACACCCCTGCCCCCATC 423
Db 660 AACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGTGTACACCCCTGCCCCCATC 719
Qy 424 CCGGATGAGTGCACCAAGAACCAAGTGCAGCTGACCTGCTGGTCAAAGGCTTCTATCC 483
Db 720 CCGGATGAGTGCACCAAGAACCAAGTGCAGCTGACCTGCTGGTCAAAGGCTTCTATCC 779
Qy 484 CAGCAGATCCCGTGGAGTGGGAGCAATGGGCGAGCCGAGAAACAATCAAGACCCAC 543
Db 780 CAGCAGATCCCGTGGAGTGGGAGCAATGGGCGAGCCGAGAAACAATCAAGACCCAC 839
Qy 544 GCCTCCCGTGGTGGACTCCGACGGCTCTCTTCTCTCATGCTCCGATGATGAGGCTCTGCACAA 603
Db 840 GCCTCCCGTGGTGGACTCCGACGGCTCTCTTCTCTCATGCTCCGATGATGAGGCTCTGCACAA 899
Qy 604 GAGCAGTGGCAGCAGGCGGAACGTCTTCTCATGCTCCGATGATGAGGCTCTGCACAA 663
Db 900 GAGCAGTGGCAGCAGGCGGAACGTCTTCTCATGCTCCGATGATGAGGCTCTGCACAA 959
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## RESULT 15

CR601777  
LOCUS full-length cDNA clone CS0CAP008YF07 of Thymus of Homo sapiens  
DEFINITION (human).  
ACCESSION CR601777  
VERSION CR601777.1 GI:50482584  
KEYWORDS HTC; CNSLT cDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
REFERENCE 1 (bases 1 to 1102)  
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Paraday Avenue  
2 (bases 1 to 1102)  
Genoscope.  
Direct Submission  
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

Search completed: March 8, 2005, 09:00:07  
Job time : 3110 secs

COMMENT  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

FEATURES  
Location/Qualifiers  
source  
1..1102  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0CAP008YP07"  
/tissue\_type="thymus"  
/plasmid="pCMVSPORT\_6"

## ORIGIN

Query Match 89.8%; Score 689.6; DB 3; Length 1102;  
Best Local Similarity 99.4%; Pred.No. 2.5e-157;  
Matches 692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 AGCAGAGCCCAATCTTGTGACAAACTCACACATGCCCGCCGACGACCTGAACCT 63  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 300 AGTTGAGCCCAATCTTGTGACAAACTCACACATGCCCGCCGACGACCTGAACCT 359  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 64 CCTGGGGGACCGTCACTCTTCTCTTCCCGCAAAACCCCAAGGACACCTCATATCTC 123  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 360 CCTGGGGGACCGTCACTCTTCTCTTCCCGCAAAACCCCAAGGACACCTCATATCTC 419  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 124 CCGGACCCCTGAGGTACATGCTGTGTGACGCTGAGCCACGAGACCCCTGAGGTCAA 183  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 420 CCGGACCCCTGAGGTACATGCTGTGTGACGCTGAGCCACGAGACCCCTGAGGTCAA 479  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||  
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DB ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 244 GCAGTACAAACAGCAGTACCGGGTGGTACGGTCTCTACCGTCTCTGACGAGACTGGCT 303  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 540 GCAGTACAAACAGCAGTACCGGTGGTGGTACGGTCTCTACCGTCTCTGACGAGACTGGCT 599  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 304 GAATGGCAGGAGTACAGTGAAGTCTTCCAAAGACCCCTCCAGCCCGCCATCGAGAA 363  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||  
QY 600 GAATGGCAGGAGTACAGTGAAGTCTTCCAAAGACCCCTCCAGCCCGCCATCGAGAA 659  
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QY 364 AACCATCTCCAAAGCCAAAGGCGAGCCCGAGAACACAGGTGTACACCTGCCCGCCATC 423  
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